7. SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: Olopade, Olufunmilayo I.

    (ii) TITLE OF INVENTION: METHYLTHIOADENOSINE PHOSPHORYLASE COMPOSITIONS AND METHODS OF USE IN THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE DISORDERS

    (iii) NUMBER OF SEQUENCES: 15

    (iv) CORRESPONDENCE ADDRESS:
        (A) ADDRESSEE: Arnold, White & Durkee
        (B) STREET: P.O. Box 4433
        (C) CITY: Houston
        (D) STATE: Texas
        (E) COUNTRY: United States of America
        (F) ZIP: 77210

    (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

    (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER: US Unknown
        (B) FILING DATE: Concurrently Herewith
        (C) CLASSIFICATION: Unknown

    (vii) PRIOR APPLICATION DATA:
        (A) APPLICATION NUMBER: US 60/000,831
        (B) FILING DATE: 02-JUL-1995
        (C) CLASSIFICATION: Unknown

    (viii) ATTORNEY/AGENT INFORMATION:
        (A) NAME: Kitchell, Barbara S.
        (B) REGISTRATION NUMBER: 33,928
        (C) REFERENCE/DOCKET NUMBER: ARSB:509

    (ix) TELECOMMUNICATION INFORMATION:
        (A) TELEPHONE: (512) 418-3000
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(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2269 base pairs

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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GAATTCCGCT CCGCACTGCT CACTCCCGCG CAGTGAGGTT GGCACAGCCA CCGCTCTGTG        60

GCTCGCTTGG TTCCCTTAGT CCCGAGCGCT CGCCCACTGC AGATTCCTTT CCCGTGCAGA       120

C ATG GCC TCT GGC ACC ACC ACC ACC GCC GTG AAG ATT GGA ATA ATT          166
  Met Ala Ser Gly Thr Thr Thr Thr Ala Val Lys Ile Gly Ile Ile
   1           5                   10                  15

GGT GGA ACA GGC CTG GAT GAT CCA GAA ATT TTA GAA GGA AGA ACT GAA        214
Gly Gly Thr Gly Leu Asp Asp Pro Glu Ile Leu Glu Gly Arg Thr Glu
              20                  25                  30

AAA TAT GTG GAT ACT CCA TTT GGC AAG CCA TCT GAT GCC TTA ATT TTG        262
Lys Tyr Val Asp Thr Pro Phe Gly Lys Pro Ser Asp Ala Leu Ile Leu
              35                  40                  45

GGG AAG ATA AAA AAT GTT GAT TGC ATC CTC CTT GCA AGG CAT GGA AGG        310
Gly Lys Ile Lys Asn Val Asp Cys Ile Leu Leu Ala Arg His Gly Arg
          50                  55                  60

CAG CAC ACC ATC ATG CCT TCA AAG GTC AAC TAC CAG GCG AAC ATC TGG        358
Gln His Thr Ile Met Pro Ser Lys Val Asn Tyr Gln Ala Asn Ile Trp
          65                  70                  75

GCT TTG AAG GAA GAG GGC TGT ACA CAT GTC ATA GTG ACC ACA GCT TGT        406
Ala Leu Lys Glu Glu Gly Cys Thr His Val Ile Val Thr Thr Ala Cys
 80                  85                  90                  95

GGC TCC TTG AGG GAG GAG ATT CAG CCC GGC GAT ATT GTC ATT ATT GAT        454
Gly Ser Leu Arg Glu Glu Ile Gln Pro Gly Asp Ile Val Ile Ile Asp
              100                 105                 110

CAG TTC ATT GAC AGG ACC ACT ATG AGA CCT CAG TCC TTC TAT GAT GGA        502
Gln Phe Ile Asp Arg Thr Thr Met Arg Pro Gln Ser Phe Tyr Asp Gly
              115                 120                 125

AGT CAT TCT TGT GCC AGA GGA GTG TGC CAT ATT CCA ATG GCT GAG CCG        550
Ser His Ser Cys Ala Arg Gly Val Cys His Ile Pro Met Ala Glu Pro
              130                 135                 140
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TTT TGC CCC AAA ACG AGA GAG GTT CTT ATA GAG ACT GCT AAG AAG CTA          598
Phe Cys Pro Lys Thr Arg Glu Val Leu Ile Glu Thr Ala Lys Lys Leu
    145             150             155

GGA CTC CGG TGC CAC TCA AAG GGG ACA ATG GTC ACA ATC GAG GGA CCT          646
Gly Leu Arg Cys His Ser Lys Gly Thr Met Val Thr Ile Glu Gly Pro
160             165             170             175

CGT TTT AGC TCC CGG GCA GAA AGC TTC ATG TTC CGC ACC TGG GGG GCG          694
Arg Phe Ser Ser Arg Ala Glu Ser Phe Met Phe Arg Thr Trp Gly Ala
            180             185             190

GAT GTT ATC AAC ATG ACC ACA GTT CCA GAG GTG GTT CTT GCT AAG GAG          742
Asp Val Ile Asn Met Thr Thr Val Pro Glu Val Val Leu Ala Lys Glu
            195             200             205

GCT GGA ATT TGT TAC GCA AGT ATC GCC ATG GCG ACA GAT TAT GAC TGC          790
Ala Gly Ile Cys Tyr Ala Ser Ile Ala Met Ala Thr Asp Tyr Asp Cys
        210             215             220

TGG AAG GAG CAC GAG GAA GCA GTT TCG GTG GAC CGG GTC TTA AAG ACC          838
Trp Lys Glu His Glu Glu Ala Val Ser Val Asp Arg Val Leu Lys Thr
    225             230             235

CTG AAA GAA AAC GCT AAT AAA GCC AAA AGC TTA CTG CTC ACT ACC ATA          886
Leu Lys Glu Asn Ala Asn Lys Ala Lys Ser Leu Leu Leu Thr Thr Ile
240             245             250             255

CCT CAG ATA GGG TCC ACA GAA TGG TCA GAA ACC CTC CAT AAC CTG AAG          934
Pro Gln Ile Gly Ser Thr Glu Trp Ser Glu Thr Leu His Asn Leu Lys
            260             265             270

AAT ATG GCC CAG TTT TCT GTT TTA TTA CCA AGA CAT TAAAGTAGCA              980
Asn Met Ala Gln Phe Ser Val Leu Leu Pro Arg His
            275             280

TGGCTGCCCA GGAGAAAAGA AGACATTCTA ATTCCAGTCA TTTTGGGAAT TCCTGCTTAA      1040

CTTGAAAAAA ATATGGGAAA GACATGCAGC TTTCATGCCC TTGCCTATCA AAGAGTATGT      1100

TGTAAGAAAG ACAAGACATT GTGTGTATTA GAGACTCCTG AATGATTTAG ACAACTTCAA      1160

AATACAGAAG AAAAGCAAAT GACTAGTAAA CATGTGGGAA AAAATATTAC ATTTTAAGGG      1220

GGAAAAAAAA AACCCCACCA TTCTCTTCTC CCCCTATTAA ATTTGCAACA ATAAAGGGTG      1280

GAGGGTAATC TCTACTTTCC TATACTGCCA AAGAATGTGA GGAAGAAATG GGACTCTTTG      1340

GTTATTTATT GATGCGACTG TAAATTGGTA CAGTATTTCT GGAGGGCAAT TTGGTAAAAT      1400

GCATCAAAAG ACTTAAAAAT ACGGACGTCC TTTGGTGCTG GGAACTCTAC ATCTAGCAAT      1460
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TTCTCTTTAA AACCATATCA GAGATGCATA CAAAGAATTA TATATAAAGA AGGGTGTTTA      1520

ATAATGATAG TTATAATAAT AAATAATTGA AACAATCTGA ATCCCTTGCA ATTGGAGGTA      1580

AATTATGTCT TAGTTATAAT CTAGATTGTG AATCAGCCAA CTGAAAATCC TTTTTGCATA      1640

TTTCAATGTC CTAAAAAGAC ACGGTTGCTC TATATATGAA GTGAAAAAAG GATATGGTAG      1700

CATTTTATAG TACTAGTTTT GCTTTAAAAT GCTATGTAAA TATACAAAAA AACTAGAAAG      1760

AAATATATAT AACCTTGTTA TTGTATTTGG GGGAGGGATA CTGGGATAAT TTTTATTTTC      1820

TTTGAATCTT TCTGTGTCTT CACATTTTTC TACAGTGAAT ATAATCAAAT AGTAAAGGGC      1880

CGTAAAAATA AAAGTGGATT TAGAAAGATC CAGTTCTTGA AAACACTGTT TCTGGTAATG      1940

AAGCAGAATT TAAGTTGGTA ATATTAAGGT GAATGTCATT TAAGGGAGTT ACATCTTTAT      2000

TCTGCTAAAG AAGAGGATCA TTGATTTCTG TACAGTCAGA ACAGTACTTG GGTGTGCAAC      2060

AGCTTTCTGA GAAAAGCTAG GTGTATAATA GTTTAACTGA AAGTTTAACT ATTTAAAAGA      2120

CTAAATGCAC ATTTTATGGT ATCTGATATT TTAAAAAGTA ATGTGAGCTT CTCCTTTTTA      2180

TGAGTTAAAT TATTTTATAC GAGTTGGTAA TTTGTGCCTT TTAATAAAGT GGAAGCTTGC      2240

TTTTTAAAAA AAAAAAAAAA GCGGAATTC                                       2269
```

(2) INFORMATION FOR SEQ ID NO:2:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 283 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: protein

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Ala Ser Gly Thr Thr Thr Thr Ala Val Lys Ile Gly Ile Ile Gly
 1               5                  10                  15

Gly Thr Gly Leu Asp Asp Pro Glu Ile Leu Glu Gly Arg Thr Glu Lys
                20                  25                  30

Tyr Val Asp Thr Pro Phe Gly Lys Pro Ser Asp Ala Leu Ile Leu Gly
                35                  40                  45
```

```
Lys Ile Lys Asn Val Asp Cys Ile Leu Leu Ala Arg His Gly Arg Gln
    50              55              60

His Thr Ile Met Pro Ser Lys Val Asn Tyr Gln Ala Asn Ile Trp Ala
65              70              75              80

Leu Lys Glu Glu Gly Cys Thr His Val Ile Val Thr Thr Ala Cys Gly
                85              90              95

Ser Leu Arg Glu Glu Ile Gln Pro Gly Asp Ile Val Ile Ile Asp Gln
        100             105             110

Phe Ile Asp Arg Thr Thr Met Arg Pro Gln Ser Phe Tyr Asp Gly Ser
        115             120             125

His Ser Cys Ala Arg Gly Val Cys His Ile Pro Met Ala Glu Pro Phe
    130             135             140

Cys Pro Lys Thr Arg Glu Val Leu Ile Glu Thr Ala Lys Lys Leu Gly
145             150             155             160

Leu Arg Cys His Ser Lys Gly Thr Met Val Thr Ile Glu Gly Pro Arg
            165             170             175

Phe Ser Ser Arg Ala Glu Ser Phe Met Phe Arg Thr Trp Gly Ala Asp
            180             185             190

Val Ile Asn Met Thr Thr Val Pro Glu Val Val Leu Ala Lys Glu Ala
        195             200             205

Gly Ile Cys Tyr Ala Ser Ile Ala Met Ala Thr Asp Tyr Asp Cys Trp
    210             215             220

Lys Glu His Glu Glu Ala Val Ser Val Asp Arg Val Leu Lys Thr Leu
225             230             235             240

Lys Glu Asn Ala Asn Lys Ala Lys Ser Leu Leu Leu Thr Thr Ile Pro
            245             250             255

Gln Ile Gly Ser Thr Glu Trp Ser Glu Thr Leu His Asn Leu Lys Asn
            260             265             270

Met Ala Gln Phe Ser Val Leu Leu Pro Arg His
            275             280
```

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 15 base pairs
        (B) TYPE: nucleic acid

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```
        (C)  STRANDEDNESS: single
        (D)  TOPOLOGY: linear


   (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:3:


GCCGTGAAGG TGAGA                                            15



(2)  INFORMATION FOR SEQ ID NO:4:

     (i)  SEQUENCE CHARACTERISTICS:
          (A)  LENGTH: 15 base pairs
          (B)  TYPE: nucleic acid
          (C)  STRANDEDNESS: single
          (D)  TOPOLOGY: linear


   (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:4:


TCTTAGATTG GAATA                                            15



(2)  INFORMATION FOR SEQ ID NO:5:

     (i)  SEQUENCE CHARACTERISTICS:
          (A)  LENGTH: 15 base pairs
          (B)  TYPE: nucleic acid
          (C)  STRANDEDNESS: single
          (D)  TOPOLOGY: linear


   (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:5:


TTTGGCAAGG TTAAT                                            15



(2)  INFORMATION FOR SEQ ID NO:6:

     (i)  SEQUENCE CHARACTERISTICS:
          (A)  LENGTH: 15 base pairs
          (B)  TYPE: nucleic acid
          (C)  STRANDEDNESS: single
          (D)  TOPOLOGY: linear


   (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:6:


ATGCAGCCAT CTGAT                                            15



(2)  INFORMATION FOR SEQ ID NO:7:

     (i)  SEQUENCE CHARACTERISTICS:
          (A)  LENGTH: 14 base pairs
```

```
          (B)  TYPE: nucleic acid
          (C)  STRANDEDNESS: single
          (D)  TOPOLOGY: linear

     (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTTGCAAGGT ATGG                                                    14


(2)  INFORMATION FOR SEQ ID NO:8:

     (i)  SEQUENCE CHARACTERISTICS:
          (A)  LENGTH: 13 base pairs
          (B)  TYPE: nucleic acid
          (C)  STRANDEDNESS: single
          (D)  TOPOLOGY: linear

     (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCATAGGCAT GGA                                                     13


(2)  INFORMATION FOR SEQ ID NO:9:

     (i)  SEQUENCE CHARACTERISTICS:
          (A)  LENGTH: 15 base pairs
          (B)  TYPE: nucleic acid
          (C)  STRANDEDNESS: single
          (D)  TOPOLOGY: linear

     (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGAGAGAGG TGTGT                                                   15


(2)  INFORMATION FOR SEQ ID NO:10:

     (i)  SEQUENCE CHARACTERISTICS:
          (A)  LENGTH: 15 base pairs
          (B)  TYPE: nucleic acid
          (C)  STRANDEDNESS: single
          (D)  TOPOLOGY: linear

     (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTCTAGGTTC TTATA                                                   15


(2)  INFORMATION FOR SEQ ID NO:11:

     (i)  SEQUENCE CHARACTERISTICS:
```

(A) LENGTH: 15 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: single
                    (D) TOPOLOGY: linear

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAGGAAGCAG TAGGT   15

     (2) INFORMATION FOR SEQ ID NO:12:

          (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 15 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: single
                    (D) TOPOLOGY: linear

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CTCTAGGTTT CGGTG   15

     (2) INFORMATION FOR SEQ ID NO:13:

          (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 15 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: single
                    (D) TOPOLOGY: linear

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AACCTGAAGG TAAGT   15

     (2) INFORMATION FOR SEQ ID NO:14:

          (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 15 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: single
                    (D) TOPOLOGY: linear

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATCCAGAATA TGGCC   15

     (2) INFORMATION FOR SEQ ID NO:15:

A 66073(1#ZD01' DOC)

(i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 15 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TTGCTTTTTT AACTC   15